

OM of: US-09-805-550-2 to: GenBank: * out_format : pfs
Date: Aug 31, 2002 7:33 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODL=frim+g2n.model -DEV=x1h
-O=/cgna2_1/USPRO.spool/US09805550/tunat_29082002.160819-275/app-query.fasta_1.897
-DB=GenBank1 -OPMT=fastap -SUFFIX=oligop2n.rge -GAPOP=4.500
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPL=0.000 -LOOPEXT=0.000
-GAPOP=6.000 -GAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
-DELOP=6.000 -DELEXT=7.000 -GAPOP=60.000 -GAPEXT=60.000
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09805550_ECGN1_1.4959 -NCPU=6 -ICPU=3 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-805-550-2
Query length: 405
Database: GenBank: *
Database sequences: 1797656
Database length: 187333701
Search time (sec): 3229.260000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

```
score_list:
Sequence      Strid Orig      ZScore      EScore Len 1522 Documentation
gb.pat:AR153819 + 405.00 7208.10 0.0 1522 AR153819 Sequence 1 from patent
gb.sts:G70483 + 38.00 662.12 1.6e-28 272 G70483 721694431F073 maize leaf
gb.sts:G71250 + 29.00 501.84 1.4e-19 251 G71250 721694431F073 maize leaf
gb.pl:AY037181 + 21.00 347.27 5.4e-11 1378 AY037181 Arabidopsis thaliana
gb.pl:AY058196 + 21.00 347.27 5.4e-11 1426 AY058196 Arabidopsis thaliana
gb.pl:LE5243875 + 20.00 329.07 5.8e-10 1498 AY243875 Lycopersicon esculent
gb.pl:AY063103 + 18.00 295.25 4.4e-08 1129 AY063103 Arabidopsis thaliana
gb.pl:AY034912 + 18.00 293.25 5.7e-08 1458 AY034912 Arabidopsis thaliana
gb.pl:DCRAD21 + 17.00 273.48 5.6e-07 1456 Y12013 Daucus carota mRNA for
gb.pl:OS063530 + 14.00 221.71 0.0005 1533 U63530 Oryza sativa cDNA for
gb.pl:AB005248 + 14.00 194.94 0.0170 83646 AB005248 Arabidopsis thaliana
gb.pl:AB005248 + 14.00 192.83 0.0223 114498 AC006341 Arabidopsis thaliana
gb.pl:F309 + 13.00 204.14 0.0052 1466 Y12014 Daucus carota mRNA for
gb.pl:DCRAD21 + 13.00 203.28 0.0058 1667 AY038562 Arabidopsis thaliana
gb.pl:AY039562 + 13.00 203.14 0.0059 1702 AR153820 Sequence 3 from patent
gb.pat:AR153820 + 13.00 178.17 0.1463 70957 AP004214 Oryza sativa chromo
gb.sts:G70483 + 13.00 177.33 0.1629 80442 AC010924 Arabidopsis thaliana
gb.pl:LE5243875 + 13.00 176.57 0.1797 90149 AC010924 Arabidopsis thaliana
gb.pl:AC010793 + 13.00 175.62 0.2029 110775 AC010793 genomic sequence for
gb.pl:ATAC021640 + 13.00 175.19 0.2144 110775 AC021640 Arabidopsis thaliana
gb.sts:G70483 + 10.00 160.07 1.49 353 AX14196 Sequence 7181 from Pat
gb.pat:AX14196 + 10.00 159.05 1.70 411 AJ770958 Lycopersicon esculent
gb.sts:G70483 + 10.00 150.01 5.01 1450 S76843 ori 3' of PGRS tandem r
gb.ba:AE006937 + 10.00 133.71 43.80 18101 AE006937 Mycobacterium tuber
gb.ba:MY0035 + 10.00 129.28 77.31 31300 AL021930 Mycobacterium tuber
gb.in:LMRL4738 + 10.00 127.95 91.79 35079 AL153930 Leishmania major F1
gb.in:AF099922 + 10.00 125.30 128.85 63599 AF099922 Caenorhabditis eleg
gb.sts:AC027633 + 10.00 118.78 297.12 168283 AC027633 Homo sapiens chro
gb.sts:AC027633 + 10.00 118.71 299.93 170143 AC027633 Homo sapiens chro
gb.sts:AC027633 + 10.00 118.20 320.06 183514 AC026924 Homo sapiens chro
gb.sts:AC027633 + 10.00 118.00 328.50 183514 AC026924 Homo sapiens chro
gb.ba:AL646078 + 10.00 116.29 409.10 203050 AL646078 Ralstonia solanace
gb.sts:AC006880 + 10.00 114.94 486.65 244239 AC006880 Caenorhabditis eleg
gb.sts:AC006880 + 10.00 114.94 486.65 298960 AC006880 Caenorhabditis eleg
gb.sts:G35919 + 9.00 142.03 15.07 362 G35919 STS h14a1268.34.5, sequ
gb.sts:G35919 + 9.00 142.03 15.07 362 G35919 STS h14a1268.34.5, sequ
gb.to:AB012865 + 9.00 137.93 25.49 668 AB012865 Mus musculus mRNA for
```

```
seq_name: gb.pat:AR153819
seq documentation block:
LOCUS AR153819 1522 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6235972.
ACCESSION AR153819
VERSION AR153819.1 GI:15121351
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Mahajan,P.B. and Taghian,L.
TITLE Maize Rad23 genes and uses thereof
JOURNAL Patent: US 6235972-A 1 22-MAY-2001.
FEATURES
source Location/Qualifiers
BASE COUNT 430 a 375 c 370 g 347 t
ORIGIN
alignment_scores:
Quality: 405.00 Length: 405
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment block:
US-09-805-550-2 x AR153819 ..
Align seg 1/1 to: AR153819 from: 1 to: 1522
1 MetLysLeuAsnValLysThrLeuLysGlyThrAspNheGluIleGluAl 17
|||||
58 ATGAAAGCTTACGTCAGACCCCTCAAGGCGACCACTTCGATCGAGCGC 107
|||||
17 aSerProAspAlaSerValAlaAspValLysArgIleIleGluThrThrg 34
|||||
108 GAGCCCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 157
|||||
34 IngLyGlnSerThrTyrrArgAlaAspGlnGlnMetLysIleTyrrGln 50
|||||
158 AAGGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 207
|||||
51 LysIleLeuLysAspGluThrThrLeuGlnLysSerGlnGlyValAla 67
|||||
208 AAAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 257
|||||
67 nSerPheLeuValIleMetLysSerLysAlaLysAlaSerSerSerGly 84
|||||
258 CAGCTCTCTTTTAAATGTTGTCACCAAGCTCAAGCAATCAAGTGGAG 307
|||||
308 CTTCACCGCTACCTACCTCAAAAGCTCTGCACTGCGCCCAACCTGCT 357
|||||
101 AlaProValAlaProAlaAlaSerValAlaArgThrProThrGlnAla 117
|||||
358 GCCCTGGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 407
|||||
117 oValaLysThrAlaGluThrAlaProProSerValGlnProGlnAlaAla 134
|||||
408 TGTTCGACGACGATGAAAGCGACCTGCAAGTGTCCAACTGAGCTGCTC 457
|||||
134 roAlaAlaThrValAlaAlaThrAspAlaAspValLysSerGlnAla 150
```

seq_name: gb_sts:G70483

seq_documentation_block: 272 bp DNA linear STS 08-JUN-2001

LOCUS G70483 721694431BP73 maize leaf DNA Zea mays STS genomic, sequence tagged site.

167 eLeuAspMetGlyGlyGlyThrTrpGluuArgAspThrValaArgAla 184
|||||
558 TCTTACATGGGTGGTGGTACATGGGAAGCTATCTGTGTTCGTGCTC 607
|||||
151 AlaSeranLeuValPheGlyAsnAsnLeuGluInThrIleGlnGlnI 167
|||||
508 GCTTCAACCTGTGTATTTGGCAACAATCTAGAACAGACTATCTCAACAAAT 557
|||||
184 euArgAlaAlaTyrAsnAsnProGluuArgAlaIleAspTyrLeuTyrSer 200
|||||
608 TACGTGCTGCATACATATAACCCCGAGAGAGCTATAGACTACCTGTATTC 657
|||||
201 GlyIleProGluAsnValGluIaGlnProValaIaArgAlaProAlaI 217
|||||
658 GGAAATTCCTGAGAAATGTGAGAGCTCAGCCTGTGGCCGAGCACCTCTGC 707
|||||
217 agIyGlnGlnThrAsnGlnGlnIaAlaIaAserProAlaGlnProAlaVala 234
|||||
708 TGGCCAAACAACAATCAGACAGCCGCATCACCCGCTCAGCCAGCAGTTG 757
|||||
234 IaLeuProValGlnProSerProAlaSerAlaGlyProAsnAlaAsnPro 250
|||||
758 CATTCCTCAGTGCAGCCATCAGCTGCTTGCAGGGGCTTATGCAAAATCCT 807
|||||
251 LeuAsnLeuPheProGlnGlyValProSerGlyGlySerAsnProGlyIya 267
|||||
808 TTGAACCTTTTCCCTCAGGCTGTCCAAATGGTGGGTCCAAACCAAGTGT 857
|||||
267 IaValProGlyIaGlySerGlyAlaLeuAspAlaLeuArgGlnLeuProG 284
|||||
858 TTGTCCAGGTGCAGGATCTGTGCTCTTATGTCCTTGCACACACTTCCAC 907
|||||
284 InPheGlnIaLeuLeuGlnLeuValaGlnAlaAsnProGlnIleLeuGln 300
|||||
908 ACTTTCAGCACTCCTTCAGTTAGTCCAGGCTATCTCAAACTTTCGAC 957
|||||
301 PrometLeuGlnIuLeuGlyLysGlnAsnProGlnIleLeuArgLeuI 317
|||||
958 CCAATGCTTCAAGAGCTAGGTAAACAACCCCAAAATCTCGGCTGTGAT 1007
|||||
317 eGlnGluAsnGlnIaGluPheLeuArgLeuValaAsnGluSerProGlnG 334
|||||
1008 TCAGGAAATCAAGCTGAGATTCTCCGCTTGGAATGAAATCTCCGAGG 1057
|||||
334 IyGlyProGlyLysAsnIleLeuGlyGlnLeuAlaIaIaValaProGln 350
|||||
1058 GTGGTCTCTGAGGGAACATACATAGTCAACTGGCACCTGCTGCGCCACA 1107
|||||
351 ThrLeuThrValThrProGluGluArgGluAlaIleGlnArgLeuGlu 367
|||||
1108 ACCCTGCACAGTTACCCAGAGCAACGGGAGGCTATCCACAGGCTCCAGG 1157
|||||
367 yMetGlyPheAsnArgGluLeuValLeuGluIuValPhePheAlaCysAsn 384
|||||
1158 AATGGGGTTCAACCGTGAAGCTTGTGTAAAGTTTCTTTGCTGATGCACAA 1207
|||||
384 yAspGluGluLeuThrAlaAsnTyrLeuLeuAspHisGlyHisGluPhe 400
|||||
1208 AGCAGCAAGAGCTTACAGCCAACTACCTCTGTGATCATGGCATGAGATT 1257
|||||
401 AspAspGlnGlnGln 405
|||||
1258 GAGCATCAGACGCAA 1272

```

ACCESSION      G70483
VERSION        G70483.1
KEYWORDS       STS.
SOURCE         Zea mays.
ORGANISM       Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 272)
Yang, Y.J., Guo, L., Ashlock, D.A., Wen, T.J., and Schnable, P.S.
AUTHORS        3 vtr sequences of maize genes
TITLE          Unpublished
JOURNAL
COMMENT
Contact: Schnable, P.S.
Schnable Laboratory
Iowa State University
6405 Agronomy Hall, Ames, IA 50011, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Primer A: TGTGGCAGAACGCTGAC
Primer B: TGTACTTGAAAGCATTCGAC
PCR Profile:
  Denaturation: 94 degrees C for 30 seconds
  Annealing: 60 degrees C for 45 seconds
  Polymerization: 72 degrees C for 90 seconds
  PCR cycles: 31
  Thermal cycler: Perkin Elmer TC
Protocol:
  Template: 10-20 ng
  Primer: each 0.5 uM
  dNTPs: each 200 uM
  Taq Polymerase: 0.05 units/ul
  Total vol: 20 ul
Buffer:
  MgCl2: 2 mM
  KCl: 50 mM
  Tris-HCl: 20 mM
  pH: 8.4.
  Location/Qualifiers
    1..272
      /organism="Zea mays"
      /strain="D8811"
      /db_xref="taxon:4577"
      /clone_lib="maize leaf DNA"
      /note="PCR products amplified from genomic DNA"
      <1..>272
BASE COUNT     64 a 59 c 78 g 71 t
ORIGIN
      STS
      BASE COUNT
Alignment_scores:
  Quality: 38.00 Length: 38
  Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-803-550-2 x G70483 ..
Align seg 1/1 to: G70483 from: 1 to: 272
364 ArgLeuGIuGIyMeGtLIyPhAsnArgLIuEuValLeuGIuValPhePh 380
|||||
13 CGGCTCGAGGGAAATGGGCTTCACCGTGAGCTTGCTGTAAGATTTCCT 62
|||||
380 eAlAcysAnLysAspGIuLeuThrAlaAsnTYrLeuDeuAspHISG 397
|||||
63 TGCATGCAACAAGACGAAGAGCTTACAGCACTACTCCTGTGATCATG 112
|||||
397 LYHISGLUPheAsp 401
|||||
113 GCCATGAGTTTGAC 126

```

seq_name: gb_sts:G71250
 seq_documentation_block: 251 bp DNA linear STS 08-JUN-2001
 LOCUS G71250 721694431F0017 maize leaf DNA Zea mays STS genomic, sequence tagged
 DEFINITION
 site: G71250
 ACCESSION G71250.1 GI:14332935
 VERSION G71250.1
 KEYWORDS STS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 251)
 Yang,Y.J., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
 3' UTR sequences of maize genes
 Unpublished
 COMMENT
 Contact: Schnable, P.S.
 Schnable laboratory
 Iowa State University
 6405 Agronomy Hall, Ames, IA 50011, USA
 Tel: 515-294-0975
 Fax: 515-294-2299
 Email: schnable@iastate.edu
 Primer A: TGCGCACAAACGCTGAC
 Primer B: TGTACTTAGAAGCATTCGAGAC
 PCR Profile:
 Denaturation: 94 degrees C for 30 seconds
 Annealing: 60 degrees C for 45 seconds
 Polymerization: 72 degrees C for 90 seconds
 PCR cycles: 31
 Thermal cycler: Perkin Elmer TC
 Protocol:
 Template: 10-20 ng
 dNTPs: each 0.5 uM
 Primer: each 200 uM
 Tag Polymerase: 0.05 units/uL
 Total vol: 20 uL
 Buffer:
 MgCl2: 2 mM
 KCl: 50 mM
 Tris-HCl: 20 mM
 pH: 8.4.

FEATURES
 source
 1..251
 /organism="Zea mays"
 /strain="DE811"
 /db_xref="taxon:4577"
 /clone_lib="maize leaf DNA"
 /note="PCR products amplified from genomic DNA"
 <1..>251
 61 a 51 c 73 g 66 t
 STS
 BASE COUNT
 ORIGIN
 alignment_scores:
 Quality: 29.00 Length: 29
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000
 alignment_block:
 US-09-805-550-2 x G71250 ..
 Align seg 1/1 to: G71250 from: 1 to: 251

360 GUAlaAlaGlnArgLeuGluGlyMetGlyPheAsnArgGluLeuValLe 376
 ||||||||||||||||||||||||||||||||||||||||||||||||
 3 GAGGTTATCCAGCGGCTCGAGGGAATGGGTTTCAACCGTAGCTTGCT 52

376 UGUlValPhePheAlaCysAsnLysAspGluLeu 388
 ||||||||||||||||||||||||||||||||||||||||||||||||
 53 AGAAGTTTTCTTTGCATGCAACAGACGAGAGAGCTC 89

seq_name: gb_PL:AY037181
 seq_documentation_block: 1378 bp mRNA linear PLN 10-JUN-2001
 LOCUS AY037181
 DEFINITION Arabidopsis thaliana unknown protein mRNA, complete cds.
 ACCESSION AY037181
 VERSION AY037181.1 GI:14335003
 KEYWORDS
 SOURCE
 ORGANISM
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 1378)
 Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P.,
 Tracy,S.E., Banh,J., Bowser,L., Carninci,P., Chung,M.K.,
 Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A.,
 Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,
 Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Pham,P.K.,
 Quach,H.L., Sakano,H., Sakurai,T., Satou,M., Seki,M., Southwick,A.,
 Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Shinozaki,K., Davis,R.W.,
 Theologis,A. and Ecker,J.R.
 Arabidopsis cDNA clones
 Unpublished
 2 (bases 1 to 1378)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P.,
 Tracy,S.E., Banh,J., Bowser,L., Carninci,P., Chung,M.K.,
 Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A.,
 Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X.,
 Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Pham,P.K.,
 Quach,H.L., Sakano,H., Sakurai,T., Satou,M., Seki,M., Southwick,A.,
 Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Shinozaki,K., Davis,R.W.,
 Theologis,A. and Ecker,J.R.
 Direct Submission
 Submitted (22-MAY-2001) Salk Institute Genomic Analysis Laboratory
 (SIGAL), Plant Biology Laboratory, The Salk Institute for
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
 USA
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
 Arabidopsis Full-length cDNA' : Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGECC (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H.,
 Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Tracy,S.E., Banh,J.,
 Bowser,L., Chung,M.K., Goldsmith,A.D., Jones,T., Karlin-Neumann,G.,
 Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,
 Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Southwick,A.,
 Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Davis,R.W., Theologis,A.,
 and Ecker,J.R.

Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
 this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
 contributed equally to this work as PIs.

FEATURES
 source
 1..1378
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /chromosome="5"
 /clone="RAFL09-12-L08(R12657)"
 /note="ecotype: Columbia"
 1..70
 71..1207
 /codon_start=1
 /product="unknown protein"
 /protein_id="AAK59766.1"
 /db_xref="GI:14335004"

```

/translation="MKIFVKTLSSGSEFEIYKPADKSDVKTATETVKGAEYPAKAKM
LIHQKVKLDETTLENNVENSFIVIMSTKASPSGASTASAPASATPOVATP
QVSAPTASVPVTSATATAAPATAVOTDVGGAASNLVAGTLESTVOOILDMG
GSMDDIVVPRALRAAFNNPRAVEVLYSGIPAOAEPVPAQAPATGBOAANPAPQ
AAAPAAATGGRNANPLNFPQMPAADAGAGNIDFLRNSQOQALAMQVANOPOIL
OPMIOELKONPOLVRLIOHOADFLRLINEVESEENVMEOLEAMQVAVTPEER
FAIERLEMGSDRAMVLEVFACNKNNEELANYLIDHHEPEDO"
3'UTR
BASE COUNT      366 a      332 c      296 g      384 t
ORIGIN

alignment_scores:
      Quality:   21.00      Length:   21
      Ratio:     1.000      Gaps:     0
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-805-550-2 x AY037181 ..
Align seg 1/1 to: AY037181 from: 1 to: 1378

292 ValGlnAlaAsnProGlnIleLeuGlnProMetLeuGlnIleuGlyly 308
|||||
875 GTACAAAGCAAAACCCACAAATTCTACAGCCCTATGCTTCAGAGCTCGGTAA 924

308 sGlnAsnProGln 312
|||||
925 ACAAAACCCCCAG 937

seq_name: gp_pl: AY058196

seq_documentation_block:
LOCUS      AY058196      1426 bp      mRNA      linear      PLN 04-NOV-2001
DEFINITION Arabidopsis thaliana unknown protein mRNA, complete cds.
ACCESSION  AY058196
VERSION    AY058196.1 GI:16648837
KEYWORDS   FLI_CDNA.
SOURCE     thale cress.
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE  1 (bases 1 to 1426)
AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
            Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
            Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
            Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,
            Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
            Tortum,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
            Davis,R.W., Theologis,A. and Ecker,J.R.
            Arabidopsis cDNA clones
            unpublished
2 (bases 1 to 1426)
TITLE     Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
JOURNAL   Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
REFERENCE Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
AUTHORS   Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,
            Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
            Tortum,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
            Davis,R.W., Theologis,A. and Ecker,J.R.
            Direct Submission
            Submitted (28-AUG-2001) Salk Institute Genomic Analysis Laboratory
            (SIGAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
            USA
COMMENT   RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA: "RIKEN
            Arabidopsis Full-length cDNA"): Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

```

```

The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H.,
Kim,C.J., Koesema,E., Meyers,M.C., Shinozaki,K., Banh,J., Bowser,L.,
Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G.,
Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,
Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A.,
Tang,C.C., Tortum,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S.,
Davis,R.W., Theologis,A., and Ecker,J.R.

Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as PIs.

FEATURES
      source
      Location/Qualifiers
          1..1426
            /organism="Arabidopsis thaliana"
            /db_xref="taxon:3702"
            /chromosome="5"
            /clone="RAFL09-10-108(R1404)"
            /note="ecotype: Columbia"
          1..78
            /codon_start=1
            /product="unknown protein"
            /protein_id="AAL25609.1"
            /db_xref="GI:16648838"
            /translation="MKIFVKTLSSGSEFEIYKPADKSDVKTATETVKGAEYPAKAKM
            LIHQKVKLDETTLENNVENSFIVIMSTKASPSGASTASAPASATPOVATP
            QVSAPTASVPVTSATATAAPATAVOTDVGGAASNLVAGTLESTVOOILDMG
            GSMDDIVVPRALRAAFNNPRAVEVLYSGIPAOAEPVPAQAPATGBOAANPAPQ
            AAAPAAATGGRNANPLNFPQMPAADAGAGNIDFLRNSQOQALAMQVANOPOIL
            OPMIOELKONPOLVRLIOHOADFLRLINEVESEENVMEOLEAMQVAVTPEER
            FAIERLEMGSDRAMVLEVFACNKNNEELANYLIDHHEPEDO"
          1216..1426
            /db_xref="taxon:3702"

BASE COUNT      377 a      343 c      301 g      405 t
ORIGIN

alignment_scores:
      Quality:   21.00      Length:   21
      Ratio:     1.000      Gaps:     0
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-805-550-2 x AY058196 ..
Align seg 1/1 to: AY058196 from: 1 to: 1426

292 ValGlnAlaAsnProGlnIleLeuGlnProMetLeuGlnIleuGlyly 308
|||||
883 GTACAAAGCAAAACCCACAAATTCTACAGCCCTATGCTTCAGAGCTCGGTAA 932

308 sGlnAsnProGln 312
|||||
933 ACAAAACCCCCAG 945

seq_name: gp_pl: LES243875

seq_documentation_block:
LOCUS      LES243875      1498 bp      mRNA      linear      PLN 28-JUL-1999
DEFINITION Lycopersicon esculentum mRNA for RAD23 homolog.
ACCESSION  AJ243875
VERSION    AJ243875.1 GI:5640110
KEYWORDS   RAD23 gene; RAD23 protein.
SOURCE     tomato.
ORGANISM   Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
            Lycopersicon.
REFERENCE  1 (bases 1 to 1498)
AUTHORS   Lemarie-Chamley,M., Petit,J., Raymond,P. and Chevalier,C.
            Analysis of gene expression during early tomato fruit development

```

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

by mRNA differential display
unpublished
2 (bases 1 to 1498)
Lemaître-Chamley M.
Direct Submission
Submitted (23-JUL-1999) Lemaître-Chamley M., Unité de Physiologie
végétale, INRA-Bordeaux, B.P. 81, 33883 Villenave d'Ornon cedex.
FRANCE

BASE COUNT	416 a	334 c	340 g	408 t
ORIGIN				

```
alignment_scores:
  Quality: 20.00
  Ratio: 1.000
  Percent Similarity: 100.000
  Length: 20
  Gaps: 0
  Percent Identity: 100.0000
```

alignment_block;
PS-09-805-550-2

Align seg 1/1 to: LES243875 from: 1 to: 1498

292 VALGlnAlaAsnProGlnIleLeuGlnPrometLeuGlnIleuGlyly 3088
948 GTGCAAGCCATCCGACGATATTGCAGCCTATGCTCCAGAGTTGGTAA 9977

seq_name: gb_p1:AY063103

seq_documentation_block:

LOCUS	1129 bp	mRNA	linear	PLN 26-NOV-2003
DEFINITION	Arabidopsis thaliana putative RAD23 protein (F20B17.8) mRNA,			

REFERENCE
1 (bases 1 to 1129)
Yamada, K., Banh, J., Banno, F., Chang, E., Dale, J. M., Goldsmith, A. D.

TITLE
JOURNAL
REFERENCE
AUTHORS

Chen, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamita, A.,
Kerlin-Neumann, G., Kawai, J., Kim, C., Kosena, E., Lam, B., Lin, J.,
Meyers, M. C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J.,
Sekuri, T., Satou, M., Seki, M., Shinn, P., Southick, A.,
Shinozaki, K., Davis, R. W., Eckert, J. R. and Theologis, A.
Full length cDNA of gene F20B17.8 (GI:7715605)
Unpublished (bases 1 to 1129)
Yamada, K., Bann, J., Banno, F., Chang, E., Dale, J. M., Goldsmith, A. D.,

TITLE Direct Submission
JOURNAL Submitted (15-NOV-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
COMMENT The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Saito,M., Kamita,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pN1 (ORF) clones using the RFL CDNA3: Yamada, K., Banh, J., Banno, F., Chang, E., Dale, J. N., Goldsmith, A. D., Lee, J. M., Yamadera, C. S., Quach, H. L., Tang, C. C., Torilum, M., Wu, H. C., Yamamura, Y., Yu, G., Yu, S., Boxer, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Kossema, E., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Nguyen, M., Palm, C. J., Shinn, P., Southwick, A., Davis, R. W., Ecker, J. R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

FEATURES
source

gene	1. .1129
	/gene="F20B17.8"
CDS	1. .1098

/note="contains two UBA PF00627 domains and is a member of the ubiquitin PF00240 family"

```

/evidence=experimental
/product="putative RAD23 protein"
/protein_id="AA134277.1"
/db_xref="GI:17104777"
/translation="MKLTVKTLLGSHFEELRVLPDPTINAVKKNIEDSGKRDNPCCGOAL
LIHHNGKYLKDETSLEVNKEVTEEGFLVWLSKSGSGSAGQASVQPVASATTSSTPRAL
PSTTQSPVPASIPAEQEQPAQOTDTLYGAASTLVSGSLSEWOOIMMGSGMDRPA
LTPFLRLAAVNNPERRAVDITVSGIIPQTAQVAVPEAQIAGSAGAPVAPAPAGSGPSSS
LDLPEETLVAAAGSGDITGLTEFLRNNDQOOLRTWYHNSPQILQPMKTLQKQNPOLL
RLIQENQAFQIDLVNPEPTGSGDEGDMFLQPEQEMPHALNVTPAEQEALQRLLEAMGPF
RALVLEAFLLACRNEELNANYLLENSGDFD"

```

```

/note="compared to genomic sequence
/replace="g"
1099. .1129
3'UTR

```

BASE COUNT	332 a	254 c	261 g	282 t
ORIGIN				

misc_difference

```

/note="compared to genomic sequence
/replace="g"
1099. .1129
3'UTR

```

BASE COUNT	332 a	254 c	261 g	282 t
ORIGIN				

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

1 (bases 1 to 1496)
Sturm, A. and Lienhard, S.
Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant
In yeast
Plant J. 13 (6), 815-821 (1998)
98345397
2 (bases 1 to 1496)
Sturm, A.
Direct Submission
Submitted (24-MAR-1997) A. Sturm, Friedrich Miescher-Institut,
Maulbeerallee 66, CH-4058 Basel, SWITZERLAND
Location/Qualifiers
1. 1496
/organism="Daucus carota"
/isolate="W01C"
/sub_species="Queen Anne's Lace"
/db_xref="taxon:4039"
63. 1211
/function="assembly factor of the complex for nucleotide
excision repair of v-damaged DNA"
/codon_start=1
/product="RAD23, isoform I"
/protein_id="CA72741.1"
/db_xref="GI:1914683"
/db_xref="SPTRMBL:003990"
/translation="MKIVTKLKGSEFIOVNPDDSVADVKRSIETNOGAAYVPAQC
MLIYGVAKDKGTTLLNNVAENSEFVIMLSKSPSGEGSTSTAAPKAPQTSAP
SVPPAVSPQPPASTLPVPAPSPAPAPATAPPSAAVGEANVYTSASLIVAGNLE
AIOOILDMGGSTMDRDYIRIVRAAFNNPERAVEYLXGIEQAEAPPVAPSPSGO
AMNPDPAPAAOPAPASAGNPANLIDFPGILPMGSMNAGAGNLDLRTMOQFOALR
AMNSPQIIOIPMCQELCKONPHMLRIQEQAPFLQINPMSGENLLHGFQALIS
VTPEROAIELELMGDFRELVEVFRCNNEELANVTLIDHMEFE"

BASE COUNT 403 a 361 c 331 g 401 t
ORIGIN

alignment_scores:
Quality: 17.00 Length: 17
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-805-550-2 x DCRAD23I ..
Align seg 1/1 to: DCRAD23I from: 1 to: 1496

295 Aa nPrGllleleugl nPr ometleugl ngl nleugl nlyugl nlna npr 311
|||||
906 ARCCCAAAATCTTGACCCCATGCTTCAGGAGTGGCAAGCAAAATCC 955
311 o 311
|
956 T 956

seq_name: gb_pl:OSU63530
seq_documentation_block:
LOCUS OSU63530 1533 bp mRNA linear PLN 07-NOV-1997
DEFINITION Oryza sativa osRAD23 mRNA, complete cds.
ACCESSION U63530
VERSION U63530.1 GI:1488296
KEYWORDS
SOURCE Oryza sativa.
ORIGIN Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehmatoidae; Oryzaceae; Oryza.
1 (bases 1 to 1533)
Schultz, T.F. and Quatrano, R.S.
Characterization and expression of a rice RAD23 gene
Plant Mol. Biol. 34 (3), 557-562 (1997)
97369378
2 (bases 1 to 1533)
REFERENCE

AUTHORS Schultz, T.F. and Quatrano, R.S.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUL-1996) Biology, University of North Carolina at Chapel Hill, CB 3280, Coker Hall, Chapel Hill, NC 27599-3280, USA
 FEATURES location/Qualifiers
 source 1. .1533
 2. /organism="Oryza sativa"
 /strain="Nipponbare"
 /db_xref="taxon:4530"
 58. .1236
 /note="RAD23 homolog"
 /codon_start=1
 /product="osRAD23"
 /protein_id="AA05841.1"
 /db_xref="GI:1488297"
 /translation="MKISVTKIGSTFOIEYDSAKYADYKRIIEETGQHIYPAEQO
 MLHQGVAKDDTLDENKVLNSEFLVIMLRQGGSSSAPATSKAPSNAPPTQVPA
 AAPSPQVAPATPVYATPVATSPPTATAPAPAPAVSEADNVOGATSNIVAGSNLEA
 TIOGILKMGCGIWDRODYLVAHLSAAPPNPEAVYILSGPEQMDIYVPPSTQPNAP
 TQSOATQVPAAPSTLSSGPNAPSLDLPQALPNASTQPAAGIGINDALRNNAQFTLLS
 LVQNAIILQPLQELGKONQOIIQLIOENQAEPLHLINPEAGDDEENLDQPEAM
 PQTAVTPPEDEALIRLEPMGFDRALVDVFAACNKDEQLAANYLLDHMEFADEGPP

BASE COUNT 414 a 395 c 333 g 391 t
 ORIGIN
 alignment_scores:
 Quality: 14.00 Length: 14
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-805-550-2 x OSU63530 ..
 Align seg 1/1 to: OSU63530 from: 1 to: 1533

23 valAlaAspValIysArgIleIleGluThrThrGlnGlyGln 36
 |||||
 124 GTTGCTGATGTGMAAGATATCGAGACTACGACGACAG 165

seq_name: gb|AF003748
 seq_documentation_block:
 LOCUS AB005248 83646 bp DNA linear PLN 27-DEC-2000
 DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, pl clone:MX110.
 ACCESSION AB005248 BA0000015
 KEYWORDS AB005248.1 GI:2264320
 SOURCE
 ORGANISM Arabidopsis thaliana (strain:Columbia) DNA, clone_11b:Mitsui P1 clone:MX110.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (sites)
 Saco,S., Kotani,H., Nakamura,Y., Kaneko,T., Asamizu,E., Fukami,M., Miyajima,N. and Tabata,S.
 Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned P1 clones
 DNA Res. 4 (3), 215-230 (1997)
 2 (bases 1 to 83646)
 Nakamura, Y.
 Direct Submission
 Submitted (02-JUL-1997) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research, 1533-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
 Address for correspondence: kos@kazusa.or.jp
 For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agg_graph.cgi?c=MX110

COMMENT
 JOURNAL MEDLINE
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL


```

CDS
    /codon_start=1
    /evidence-not_experimental
    join(45089..45677,46843..47158,47312..47452,47544..47871)
    /note="contains similarity to non-LTR retroelement reverse
    transcriptase
    gene_id:MX110.11"
    /codon_start=1
    /pseudo
    /evidence-not_experimental
    48978..49433
    /note="gene_id:MX110.12
    unknown protein"
    /codon_start=1
    /evidence-not_experimental
    /protein_id="BAB09352.1"
    /db_xref="GI:9758818"
    /db_xref="GI:9758818"
    /translation="MNDSMKRAYSAVECKERRSSNGEPTREOSKHAMTAKAR
    MNYKESMKPIPPKRSKSLMILISLRKKEDTODDNNNTTYVEKEKEKGVONIRE
    NAEMLSSKVEEPMHLYEEEMTFAPFGWMQRYDAVMSGKSMFN"
    complement(join(50633..50872,51043..51177,51268..51438))
    /note="gene_id:MX110.13
    sp|P10798"
    /codon_start=1
    /evidence-not_experimental

alignment_scores:
    Quality: 14.00      Length: 14
    Ratio: 1.000        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
    US-09-805-550-2 x AB005248 ..

Align seg 1/1 to: AB005248 from: 1 to: 83646

299 LeuGlnProMetLeuGlnGluLeuGlyLysGlnAsnProGln 312
|||||
80121 TTTCAGCCTATGCTTCAGAGCTCGTAAACAAACCCCGAG 80162

seq_name: gb_pl:F309

seq_documentation_block:
LOCUS      F309      114498 bp      DNA      linear      PLN 02-JUN-1999
DEFINITION Arabidopsis thaliana chromosome 1 BAC F309 sequence, complete
sequence.
ACCESSION  AC006341
VERSION     AC006341.2
KEYWORDS    HG:4887257
SOURCE      HG:
ORGANISM    Thale cress.
             Arabidopsis thaliana
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 114498)
Vysotskaya,V.S., Schwartz,J., Yu,G., Tortum,M., Lenz,C., Liu,S.,
Lee,J., Li,J., Kremetskaia,I., Liu,A., Luros,J., Gonzalez,A.,
Altafi,H., Araujo,R., Chao,Q., Conn,L., Conway,A.B., Dunn,P.,
Hansen,N., Hutzar,L., Kim,C., Palm,C., Rowley,D., Shinn,P.,
Walker,M., Davis,R.W., Becker,J.R., Federspiel,N.A. and Theologis,A.
The sequence of BAC F309 from Arabidopsis thaliana chromosome 1
Unpublished (1999)
2 (bases 1 to 114498)
Theologis,A.
REFERENCE   Direct Submission
AUTHORS     Submitted (11-JAN-1999) Plant Gene Expression Center, 800 Buchanan
JOURNAL     Street, Albany, CA 94710, USA
3 (bases 1 to 114498)
Theologis,A.
REFERENCE   Direct Submission
AUTHORS     Submitted (25-MAY-1999) Plant Gene Expression Center, 800 Buchanan
JOURNAL     Street, Albany, CA 94710, USA
4 (bases 1 to 114498)

```

```

AUTHORS     Theologis,A.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUN-1999) Plant Gene Expression Center, 800 Buchanan
COMMENT     St., Albany, CA 94710, USA
            On May 25, 1999 this sequence version replaced gi:1139327.
            The sequence of BAC F309 from Arabidopsis thaliana chromosome 1.
FEATURES
source
1..114498
    /organism="Arabidopsis thaliana"
    /cultivar="Columbia"
    /db_xref="taxon:3702"
    /chromosome="1"
    /clone="F309"
    246..901
    /gene="F309.1"
    join(246..275,353..462,608..692,785..901)
    /gene="F309.1"
    /note="Similar to gb|Y12014 RAD3 protein isoform II from
    Daucus carota. This gene is probably cut off. EST
    gb|AA651284 comes from this gene."
    /codon_start=1
    /evidence-not_experimental
    /protein_id="AAD34675.1"
    /db_xref="GI:4966345"
    /translation="MVNSNPQILQPMLEPLGKONPOLRLIDBNQAEPLQLNEPYEG
    SPGDVDFIDQPEMPHSVNTPEQESIERLEAMGFDAIVIEAFLSCDRNEELAN
    YLEHSADPED"
    complement(1361..2444)
    /gene="F309.2"
    complement(join(1361..1387,1506..1625,1899..2444))
    /gene="F309.2"
    /note="ESTs gb|T04357 and gb|AA595092 come from this
    gene."
    /codon_start=1
    /evidence-not_experimental
    /protein_id="AAD34673.1"
    /db_xref="GI:4966342"
    /translation="MGLNSKAEVANSRKNAABAEOKROTREKEQYWEAPGPKSKA
    YKREEEAEKKAETAKLEAKRLAEQEELEKALKDKRANRYTVPVKYTEEL
    IRRREDOVALAKAEDSKKOTRMAGEDEYEMVLTNTNDDSLIEAHVTDEALR
    ITVSDNLPYDRHPERKLKASFAYEEVELPRKSEKRGILTHQYKDLIKMKMKSSDN
    PINQAAAAANAE"
    3662..3562
    /gene="F309.3"
    join(3662..3916,4107..4475,4552..4669,4755..4978,
    5053..5562)
    /gene="F309.3"
    /note="Is a member of Pf100481 Protein phosphatase 2C
    family."
    /codon_start=1
    /evidence-not_experimental
    /protein_id="AAD34674.1"
    /db_xref="GI:4966343"
    /translation="MGLCSKIDKTRKETGATSTATTYVEROSSGRLLRPRLDYSYG
    EISEIQVGRVGNSSSEIATITQOGKGTQDMALWENFCSBDVLCGVFEGH
    GPGHNVSKVRHDMLEPFTLSQIKTTSQGEQSSKNGLSAPICVDEWCELOCEK
    DRLPEPMYLPKRLALTKCOQDKELKMHPIINCSCSTTSYTVYKQKDLVGNIG
    DRAVLATBDONALVAVOYLTDLKDLDESESRHRCGRVYATLADDEEVANVWLPN
    SPSFGAMARQAFGFLKDYGLISVDYHRTREDOYITLADDSVWYVLSKEAYD
    IVASAPRPARAAVYDVAVRNRLKTPPSKNDCAVYVLFLEDTSAAGTVESETVN
    HSHESTESVYITTSKADAKKEEASTETETVPWETKEEKEPTESCRISKTTTAE
    ISVKDEMSALEGLRVNSLSIPRFSGELRSSSRMWL"
    complement(10192..11349)
    /gene="F309.4"
    complement(join(10192..10323,10518..10562,10642..10742,
    10834..11039,11135..11349))
    /gene="F309.4"
    /note="ESTs gb|F15498, gb|H37515, gb|T41906, gb|T22448,
    gb|W43356 and gb|T20739 come from this gene."
    /codon_start=1
    /evidence-not_experimental
    /protein_id="AAD34675.1"
    /db_xref="GI:4966344"

```

gene
CDS
/translation="MASSSDSWARAYNEALKSEINGMISERSSSAVTGPDQRAS
AIRKTIIFGNKIDSLQSLAEIHGPISEKENRRDWMGNLSKANQMANLNMNS
FANDSLIGPIDKPDQMSRYTGNDGIVGYOQVNRQEDQEGLEQETVMSTRKHA
LAVSELDQTLRIDLDYHVDYDSRLRRVOKSLAVMNKMRSGCCSMMLSVLGI
VGLAVVIMMLVKVM"
/gene="F309.5"
/join(11987..12044,12084..12224,12408..12954,13133..13706)
/gene="F309.5"
/note="Contains two PF101344 Kelch motif domains."
/codon.start=1
/evidence=not_experimental
/protein_id="A03467.1"
/db_xref="GI:4966346"
/translation="MPVSVSLPCQNEFLSDFSVSIYNGVFGSKVINFARFMC
SKASRSGSEDFEITISRVRGSCILPDALRCIAKLSHGVLGECVSRGRDLYVAC
DYCYKARNMGSMFLFVTERSKNOMVAYADPEADRMHPYPRTRAVODGMSHAFAC
CVSNCLIVIGGCYVAFSPFHOKPVYTKDMREDPKKMKVAVSMRPTTHACVS
VSGKTVYAGRNLTSHNGITSAEYTDYADRMETLPMAPRQDCSGLSTRGCTHVS
DQGFANQSEVEFNPDMTSTVEDVWPFSAQFAVQVKNDRVYTYVMGSLIK
TRDDEGMVNGSVPSVLPNHPRELAFGYGFALRNELLYVIGKRWKEESGAGR
FDIVLFFVAVCBPLDRPLMWRKPMPCIPAGCSIIICVSLSESSP"
/complement(1417..17027)
/gene="F309.6"
complement(join(14717..15924,15993..16097,16178..17027))
/gene="F309.6"
/note="Similar to gb|A012423 wall-associated kinase 2
from Arabidopsis thaliana."
/codon.start=1
/evidence=not_experimental
/protein_id="A03467.1"
/db_xref="GI:4966347"
/translation="MGVDRFLVVMILLRICEYAAASTEPFLANRCSNDCGVSVY
/PFGKCYKMKWEIVKSSSDQPTLLPRIRAVTSTNLGRDPSIYVNFYIOS
PLKHSGCPNDRGSSSLNKGSEFISENNKFAVCNNKAFNATVGLQVGETTC
GNEIRSKYKANTSGVCCOMTIPPLLOVAPYATEKLEQCOVAFLOFETIS
GSLTPELMESSEYTIEMELRDLSTMTSKYREKTPALISTSGCLLIFGMA
YIRGGCODIDECBPHLKRCGRKCVAVLGSYREKTPALISTSGCLLIFGMA
LICKANKRRVAVAKRKFQFQNGGLQDQTSFLHGSVNRKYFSSNDLEADTFNA
SRILGOGGQGVYKGLMDGMIYAVKSKALKENLEFNEILLQINRNVKIL
GCCLEVEPLVYEFIPNMLFHLNPSDEPMSWELFCLICEVADALSYLSAVS
IPYHRDVTNLLDEKIRAKVSDGISISVADIDHLLTYGDTIGYGVDELQSN
HFTGSDVYSFVGLLELLEKRPVSLRQEVSLGAYLEARNRNLHEILLARIK
EECDREVLAVAKLARCLSLNSHRTMDVFTELDRMOSKRGTGSOANQGEHNAH
IQIAMPESKSLSTSPNIVNSFSIDTFLPMHKQ"
/18899..23154
/gene="F309.7"
/join(18899..21385,21458..21538,21719..21871,21997..22160,
22371..22418,22491..22613,22684..22771,22955..23154)
/gene="F309.7"
/note="Contains PF100069 Eukaryotic protein kinase domain.
ESTs gb|H37741, gb|T43005 and gb|A1100340 come from this
gene."
/codon.start=1
/evidence=not_experimental
/protein_id="A03467.1"
/db_xref="GI:4966348"
/translation="MDNRPPHPQOHAMEGVYNDSPQGFPPDQTLNANVRNP
ADVPGIHYISIQGEERFLEFLDRVYSQSNIAAGDINPYGNGHSGEFGSV
SRMSWNGIRQYERTNPVHEFGNKGHLSHAPSLACDRTSGNFGASSASVS
LTKAVKYGSGFKILPRGDSKLRVYGSGTHITISIKDLSMELROKRYEYRTH
VKYQLRGEDDALVYSCDDDLNMEYEMERKGSQKLRLMFLSVSDIDLALVY
NKSDBSEFYVAVNDMDLGSNSNLTNLCDSSANLLELDVRNTEGINDVPSOL
TGIDPOOSMOYSEAPTSFAQYPOIPIINGAEFOQAVPNNATLQYASNPSSSV
HYPOSILPNTLOYPOSISSSYGLYPOYGEFOFQADNHNSSVSTIPPCQP
YHPGITOQNAPOVEEPPNKETKYDYEPERHLLANHONPPOADQTEVNRBP
SVATYVSOADAHLPPRBDTRONTPYKSTYDADATVTDVYSGEDQDLSGSGCG
LVHTDSNLIIDYPERLOPTRRYRSEIRPREQLEMLRLSKSDLSQFLMSP
QASTGOEPKAEAGISHEDSHVNDENISGVNVAENELDKRTVSGGILETARNL
QSVTERSHDIPKQTSVGLIDINDFPDQFLSEIFAKALSDMPAMYQDAGG
VSLVNHNDPKNMSYFRNLADEQSDRDVAYIDRTPEPSMDMEGCIARHQAPLYT
ENRVDPMQKTESSEFPAVYENLRTSDCEDEKSETRNAGLIPVPGSLADYDSGLQ
IIMNDLEELKEIGSGTFGTVHGMKRGSDVALIKRIKSCFAGSSQERLTGEFWE

gene
CDS
complement(23491..25496)
/gene="F309.8"
complement(join(23491..23643,23824..23922,24023..24104,
24189..24392,24473..24795,24882..25496))
/gene="F309.8"
/note="Similar to gb|L13612 DEAD-box protein (dbp45A) from
Drosophila melanogaster and is a member of PF100270
DEAD/DEAH box helicase family."
/codon.start=1
/evidence=not_experimental
/protein_id="A03468.1"
/db_xref="GI:4966350"
/translation="MEPTPEEGCITIMSKRKNPTVYNISQKIDSDQNTPOFEK
FTNPNPSDITTSANFEGGLAEAVAECEKELGRKPTPVQTHCPVILAGRDVGLA
QTGSGKTAFAFLPIHLRAEDPYGVFALVYTPGRILVLENNPDVPPVSRKFLVLEADVLVY
VGGMDMLQOTWSLVSRPHVITTPGRILVLENNPDVPPVSRKFLVLEADVLVY
GFODELRTIFQCLPKSRQTLFSAVMTSNLOALLEHSSNKAYFEAYEGKTVDTLQ
OFIFEDDAKELVYLHILISQMEDKGISAMIFVSTCRQORLSIMLELEVENIAMS
LNSQSMRLSALSKRSKVPILLATDVASRGDLIPYDLYNTVIDPDRDPRVYRVR

alignment_scores:

Quality:	14.00	Length:	14
Ratio:	1.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:

US-09-805-550-2 x F309 ..

Align seg 1/1 to: F309 from: 1 to: 114498

299 leuGlnPrometleuGlnIleuGlnIleuGlnAaProGln 312
|||||
347 TTRACAGCCTATGCTTCAAGAGCTCGGAAAGACAGACCCCA 388

seq_name: gb_pl:DCRAD23II

seq_documentation_block:

LOCUS	DCRAD23II	1466 bp	mRNA	linear	PLN 28-JAN-1999
DEFINITION	Daucus carota mRNA for RAD23 protein, isoform II.				
ACCESSION	Y12014				
VERSION	Y12014.1				
KEYWORDS	isoform II; RAD23 (ubiquitin-like protein involved in UV excision repair).				

SOURCE

ORGANISM

Daucus carota

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; eunasterids II; Apiales; Apiaceae; Daucus.

REFERENCE

1 (bases 1 to 1466)

Sturm, A. and Lienhard, S.

Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant

in yeast

JOURNAL

Plant J. 13 (6), 815-821 (1998)

MEDLINE

98345997

2 (bases 1 to 1466)

Sturm, A.

Direct Submision

Submitted (24-MAR-1997) A. Sturm, Friedrich Miescher-Institut,
Maulbeerallee 66, CH-4058 Basel, SWITZERLAND

FEATURES

source

1..1466

/organism="Daucus carota"

/isolate="W01C"

/sub_species="Queen Anne's lace"

/db_xref="taxon:4039"

40..1179

/function="assembly factor of the complex for nucleotide
excision repair of V-damaged DNA"

ORIGIN

alignment_scores: length: 13
 quality: 13.00
 ratio: 1.000
 gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-805-550-2 x AR153820 ..

Align seg 1/1 to: AR153820 from: 1 to: 1702

182 ArgAlaLeuArgAlaAlaTyrAsnAsnProGluArgAla 194
 ||||||||||||||||||||||||||||||||||||||||
 604 AGGGCTCTCCGTGCCGCTTACAAACAACCCCGAACGTGCT 642